```
==============================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2008; month=10; day=29; hr=14; min=2; sec=36; ms=339; ]
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**************************************************************
Reviewer Comments:
<210>   3
<211>   6
<212>   PRT
<213>   artificial

<220>
<223>   distinctive fragment

<400>   3

Ile Ala Arg Ile Ile Gly
1               5


The above <223> response is an insufficient explanation for "Artificial
Sequence":  please give more information regarding the source of the
"distinctive fragment."  Same type of insufficient explanations in
Sequences 4-11.
**************************************************************
```

Application No: 10578493   Version No: 3.0

Input Set:

Output Set:

Started:	2008-09-29 16:55:12.825
Finished:	2008-09-29 16:55:14.100
Elapsed:	0 hr(s) 0 min(s) 1 sec(s) 275 ms
Total Warnings:	32
Total Errors:	0
No. of SeqIDs Defined:	36
Actual SeqID Count:	36

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)

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         Input Set:


        Output Set:



           Started:   2008-09-29 16:55:12.825
          Finished:   2008-09-29 16:55:14.100
           Elapsed:   0 hr(s) 0 min(s) 1 sec(s) 275 ms
   Total Warnings:    32
     Total Errors:    0
No. of SeqIDs Defined:  36
 Actual SeqID Count:    36
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Error code   Error Description

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       This error has occured more than 20 times, will not be displayed
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ctgcggctgc ccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt   180

gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc   240

gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca   300

gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca   360

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag   420

ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt   480

gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg   540

gggctggcct atgctgagat tgccaggatc attggaggta tcgaccactc gctgtacaca   600

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gccctcttca tgctgccact ctgcctcatg gtgtgtcagt ggcgctgcct ccgctgcctg   1320

cgccagcagc atgatgactt tgctgatgac atctccctgc tgaagtga   1368

<210>   2
<211>   455
<212>   PRT
<213>   Homo sapiens

<400>   2

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
             20   25   30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
         35   40   45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
     50   55   60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65   70   75   80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                85   90   95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
            100   105   110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115   120   125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
    130   135   140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145   150   155   160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
                165   170   175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Ile Ile Gly
                180   185   190

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
                195   200   205

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
    210   215   220

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
225   230   235   240

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
                245   250   255

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
                260   265   270

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
                275   280   285

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
    290   295   300

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
305   310   315   320

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
                325   330   335

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
                340   345   350

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
        355   360   365

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
    370   375   380

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
385   390   395   400

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
                405   410   415

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
                420   425   430

Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
        435   440   445

Asp Asp Ile Ser Leu Leu Lys
    450   455

<210>   3
<211>   6
<212>   PRT
<213>   artificial

<220>
<223>   distinctive fragment

<400>   3

Ile Ala Arg Ile Ile Gly
1   5

<210>   4
<211>   7
<212>   PRT
<213>   artificial

<220>
<223>   distinctive fragment

<400>   4

Glu Ile Ala Arg Ile Ile Gly
1   5

<210>   5

<211> 8
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 5

Glu Ile Ala Arg Ile Ile Gly Gly
1   5

<210> 6
<211> 8
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 6

Ala Glu Ile Ala Arg Ile Ile Gly
1   5

<210> 7
<211> 9
<212> PRT
<213> artificial

<220>
<223> AEIARIIGG

<400> 7

Ala Glu Ile Ala Arg Ile Ile Gly Gly
1   5

<210> 8
<211> 10
<212> PRT
<213> artificial

<220>
<223> distinctive fragment

<400> 8

Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
1   5   10

<210> 9
<211> 9

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<212>   PRT
<213>   artificial

<220>
<223>   distinctive fragment

<400>   9

Tyr Ala Glu Ile Ala Arg Ile Ile Gly
1               5


<210>   10
<211>   10
<212>   PRT
<213>   artificial

<220>
<223>   distinctive fragment

<400>   10

Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly
1               5                   10


<210>   11
<211>   11
<212>   PRT
<213>   artificial

<220>
<223>   distinctive fragment

<400>   11

Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
1               5                   10


<210>   12
<211>   18
<212>   DNA
<213>   artificial

<220>
<223>   probe

<400>   12
attgccagga tcattgga                                             18


<210>   13
<211>   10
<212>   DNA
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<220>
<223> primer

<400> 13
aggcatcctg   10

<210> 14
<211> 10
<212> DNA
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<220>
<223> primer

<400> 14
gggctggcct   10

<210> 15
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<212> DNA
<213> artificial

<220>
<223> primer

<400> 15
atgctgagat   10

<210> 16
<211> 6
<212> DNA
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<220>
<223> primer

<400> 16
tgccag   6

<210> 17
<211> 6
<212> DNA
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<220>
<223> primer

<400> 17
gatcat   6

<210> 18
<211> 10

<212> DNA
<213> artificial

<220>
<223> primer

<400> 18
tggaggtatc   10

<210> 19
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<220>
<223> primer

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gaccactcgc   10

<210> 20
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<212> DNA
<213> artificial

<220>
<223> primer

<400> 20
tgtacacagg   10

<210> 21
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<220>
<223> primer

<400> 21
cagtctctgg   10

<210> 22
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<220>
<223> primer

<400> 22
caggat   6

<210> 23
<211> 8
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<220>
<223> primer

<400> 23
ccaggatc   8

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<212> DNA
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<220>
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gccaggatca   10

<210> 25
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<212> DNA
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<220>
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<400> 25
attgccagga tcattgga   18

<210> 26
<211> 21
<212> DNA
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<220>
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<400> 26
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<210> 27
<211> 19
<212> DNA
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<220>
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<400> 27
agttgtgcat gggagcgag   19

<210> 28
<211> 19
<212> DNA
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<220>
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<400> 28
cccgcagacg ctcaacatc   19

<210> 29
<211> 21
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<220>
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<400> 29
cagcgagtgg tcgatacctc c   21

<210> 30
<211> 24
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<220>
<223> primer

<400> 30
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<210> 31
<211> 33
<212> DNA
<213> artificial

<220>
<223> primer

<400> 31
ggggaattca cttcagcagg gagatgtcat cag   33

<210> 32
<211> 10
<212> PRT
<213> artificial

<220>
<223> fluorogenic App-based peptide MCA

<400> 32

Ser Glu Val Asn Leu Asp Ala Glu Phe Lys
1   5   10

<210> 33
<211> 9
<212> PRT
<213> artificial

<220>
<223> BACE inhibitor III

<220>
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<222> (5)..(5)
<223> Xaa is statine

<400> 33

His Glu Val Asn Xaa Val Ala Glu Phe
1   5

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> beta-secretase cleavage site in APP

<400> 34

Glu Val Lys Met Asp Ala Glu
1   5

<210> 35
<211> 8
<212> PRT
<213> Homo sapiens

<400> 35

Leu Val Asn Met Ala Glu Gly Asp
1   5

<210> 36
<211> 501
<212> PRT

<213> Homo sapiens

<400> 36

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Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1               5                   10                  15


Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
                20                  25                  30


Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
            35                  40                  45


Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
        50                  55                  60


Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65                  70                  75                  80


Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
                85                  90                  95


Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
                100                 105                 110


Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
        115                 120                 125


Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
        130                 135                 140


Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145                 150                 155                 160


Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
                165                 170                 175


Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
                180                 185                 190


Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
                195                 200                 205


Asn Leu Phe Ser Leu Gln Leu Cys Cys Ala Gly Phe Pro Leu Asn Gln
```

```
              210                       215                       220


Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225                 230                 235                 240


Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
                    245                 250                 255


Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
                260                 265                 270


Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
            275                 280                 285


Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
        290                 295                 300


Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305                 310                 315                 320


Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
                325                 330                 335


Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
                340                 345                 350


Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
            355                 360                 365


Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
        370                 375                 380


Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385                 390                 395                 400


Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
                405                 410                 415


Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
            420                 425                 430


Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
        435                 440                 445
```

```
Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
    450                 455                 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465                 470                 475                 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
                485                 490                 495

Ile Ser Leu Leu Lys
            500
```